



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 17, 2022 – 08:04 AM EST

PDB ID : 7UKW
Title : EGFR(T790M/V948R) in complex with Lazertinib (YH25448)
Authors : Pham, C.D.; Heppner, D.E.
Deposited on : 2022-04-02
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

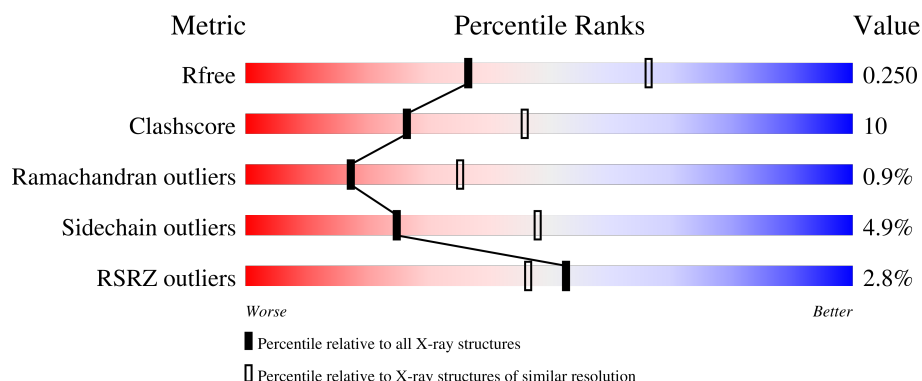
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	328	<div> <div>2%</div> <div>78%</div> <div>14%</div> <div>7%</div> </div>
1	B	328	<div> <div>4%</div> <div>60%</div> <div>28%</div> <div>11%</div> </div>
1	C	328	<div> <div>2%</div> <div>70%</div> <div>17%</div> <div>12%</div> </div>
1	D	328	<div> <div>0%</div> <div>67%</div> <div>22%</div> <div>9%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9736 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

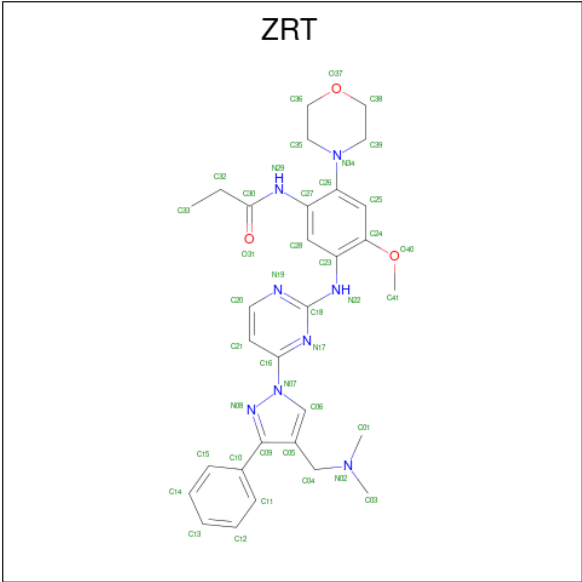
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	300	Total	C	N	O	S	0	1	0
			2421	1556	411	436	18			
1	A	306	Total	C	N	O	S	0	0	0
			2451	1574	417	442	18			
1	B	292	Total	C	N	O	S	0	0	0
			2336	1499	395	423	19			
1	C	287	Total	C	N	O	S	0	1	0
			2314	1489	394	413	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is N-[5-[[[(4P)-4-{4-[(dimethylamino)methyl]-3-phenyl-1H-pyrazol-1-yl}pyrimidin-2-yl]amino}-4-methoxy-2-(morpholin-4-yl)phenyl]propanamide (three-letter code: ZRT) (formula: C₃₀H₃₆N₈O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			41	30	8	3		
2	C	1	Total	C	N	O	0	0
			41	30	8	3		

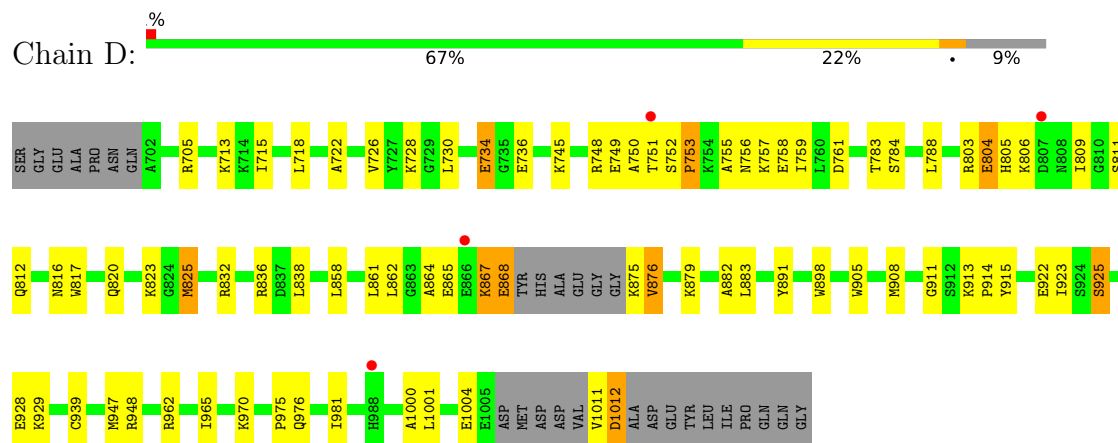
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	34	Total	O	0	0
			34	34		
3	A	36	Total	O	0	0
			36	36		
3	B	25	Total	O	0	0
			25	25		
3	C	37	Total	O	0	0
			37	37		

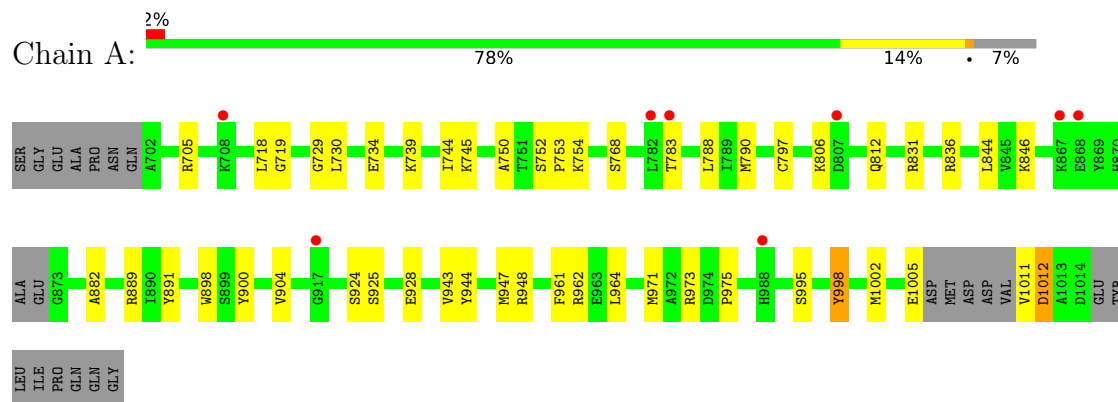
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

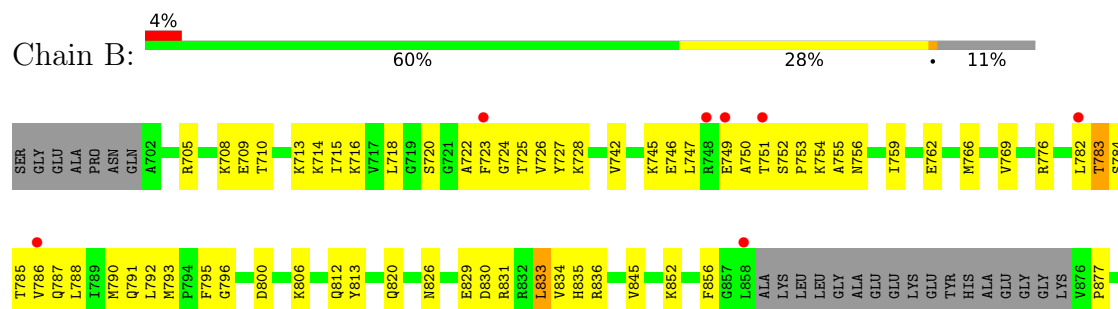
• Molecule 1: Epidermal growth factor receptor

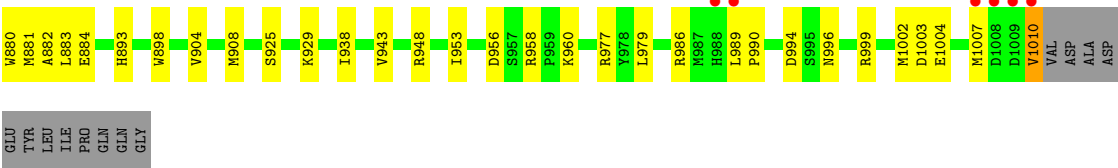


• Molecule 1: Epidermal growth factor receptor

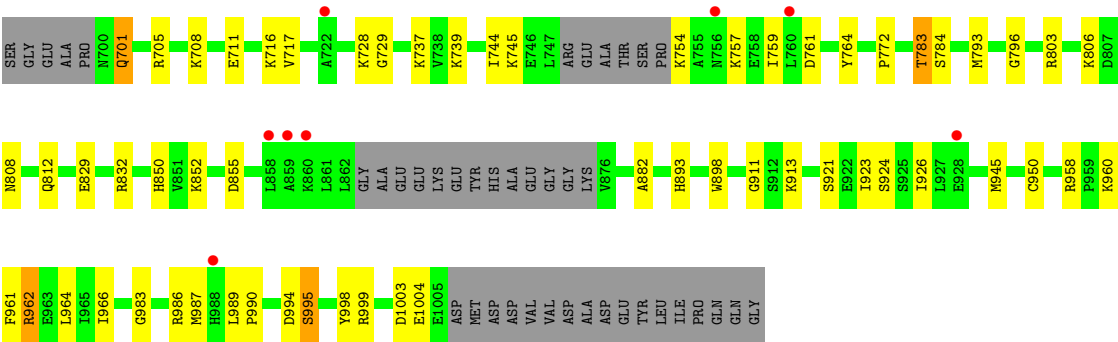


• Molecule 1: Epidermal growth factor receptor





● Molecule 1: Epidermal growth factor receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.05Å 101.80Å 87.35Å 90.00° 102.37° 90.00°	Depositor
Resolution (Å)	65.35 – 2.60 65.39 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.8 (65.35-2.60) 92.5 (65.39-2.59)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.27 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.195 , 0.250 0.195 , 0.250	Depositor DCC
R_{free} test set	1992 reflections (5.31%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9736	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.28 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.9515e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZRT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.31	0/2504	0.51	0/3384
1	B	0.36	0/2387	0.56	0/3231
1	C	0.31	0/2363	0.49	0/3195
1	D	0.35	0/2472	0.54	0/3339
All	All	0.33	0/9726	0.53	0/13149

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2451	0	2485	29	0
1	B	2336	0	2355	70	0
1	C	2314	0	2357	43	0
1	D	2421	0	2470	65	0
2	B	41	0	0	3	0
2	C	41	0	0	1	0
3	A	36	0	0	2	0
3	B	25	0	0	3	0
3	C	37	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	34	0	0	2	0
All	All	9736	0	9667	199	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (199) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:867:LYS:HE3	1:D:875:LYS:HG2	1.24	1.18
1:D:867:LYS:HE3	1:D:875:LYS:CG	1.76	1.15
1:C:962:ARG:NH2	1:C:966:ILE:HD11	1.65	1.11
1:C:754:LYS:HG2	1:C:759:ILE:HG13	1.31	1.09
1:D:722:ALA:HB1	1:D:875:LYS:HD2	1.36	1.06
1:D:867:LYS:CE	1:D:875:LYS:HG2	1.88	1.03
1:C:962:ARG:HH21	1:C:966:ILE:HD11	0.86	1.03
1:D:867:LYS:O	1:D:876:VAL:HG13	1.59	1.01
1:C:962:ARG:HH21	1:C:966:ILE:CD1	1.73	1.00
1:A:729:GLY:HA3	1:A:744:ILE:HD11	1.45	0.99
1:B:833:LEU:HD22	1:B:856:PHE:HZ	1.32	0.94
1:D:867:LYS:O	1:D:876:VAL:CG1	2.16	0.92
1:A:729:GLY:HA3	1:A:744:ILE:CD1	2.05	0.86
1:B:752:SER:HB3	1:B:756:ASN:OD1	1.80	0.82
1:D:867:LYS:HE3	1:D:875:LYS:HG3	1.61	0.81
1:B:1007:MET:HE3	3:B:1223:HOH:O	1.80	0.80
1:B:999:ARG:HH21	1:B:1007:MET:HG2	1.48	0.78
1:C:812:GLN:CG	3:C:1215:HOH:O	2.33	0.77
1:C:986:ARG:HG3	1:C:986:ARG:HH11	1.50	0.76
1:D:722:ALA:HB1	1:D:875:LYS:CD	2.13	0.76
1:C:701:GLN:HA	1:C:764:TYR:CE1	2.20	0.75
1:C:986:ARG:HG3	1:C:986:ARG:NH1	2.00	0.75
1:B:752:SER:CB	1:B:756:ASN:OD1	2.34	0.74
1:B:833:LEU:HD22	1:B:856:PHE:CZ	2.21	0.74
1:D:867:LYS:HZ1	1:D:875:LYS:HE3	1.53	0.73
1:B:709:GLU:OE2	1:B:783:THR:CB	2.35	0.73
1:D:868:GLU:HG3	1:D:876:VAL:HG21	1.72	0.71
1:C:923:ILE:HD13	1:C:926:ILE:HD11	1.71	0.71
1:B:999:ARG:NH2	1:B:1007:MET:HG2	2.06	0.70
1:B:999:ARG:HH21	1:B:1007:MET:CG	2.06	0.69
1:C:754:LYS:HG2	1:C:759:ILE:CG1	2.16	0.69
1:C:983:GLY:O	1:C:986:ARG:HG2	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:875:LYS:N	1:D:875:LYS:HD3	2.10	0.66
1:A:973:ARG:NH1	1:A:1012:ASP:O	2.25	0.66
1:D:832:ARG:HH11	1:D:832:ARG:HG3	1.61	0.66
1:A:730:LEU:HD22	1:A:739:LYS:HB2	1.78	0.66
1:D:913:LYS:HD2	1:D:914:PRO:HD2	1.78	0.66
1:D:726:VAL:HG22	1:D:745:LYS:HG3	1.77	0.65
1:D:925:SER:O	1:D:929:LYS:HE2	1.95	0.65
1:C:701:GLN:HA	1:C:764:TYR:HE1	1.60	0.65
1:D:756:ASN:ND2	3:D:1101:HOH:O	2.21	0.65
1:B:831:ARG:HB2	1:B:833:LEU:HD12	1.78	0.65
1:C:995:SER:O	1:C:999:ARG:HG3	1.97	0.65
1:C:812:GLN:HG2	3:C:1215:HOH:O	1.96	0.64
1:C:812:GLN:HG3	3:C:1215:HOH:O	1.94	0.63
1:B:728:LYS:HG2	1:B:792:LEU:HD11	1.79	0.63
1:B:745:LYS:HE2	2:B:1101:ZRT:C14	2.29	0.63
1:B:724:GLY:H	1:B:745:LYS:HZ1	1.46	0.63
1:B:834:VAL:HG12	1:B:836:ARG:HG3	1.81	0.63
1:B:759:ILE:HD13	1:B:786:VAL:HG21	1.80	0.63
1:B:713:LYS:HD2	1:B:715:ILE:HD11	1.81	0.62
1:A:943:VAL:HG22	1:A:971:MET:CE	2.28	0.62
1:B:989:LEU:HG	1:B:990:PRO:HD2	1.83	0.61
1:A:1011:VAL:N	3:A:1106:HOH:O	2.34	0.60
1:B:723:PHE:CB	1:B:745:LYS:HZ1	2.16	0.59
1:D:879:LYS:HD3	1:D:915:TYR:HB2	1.83	0.59
1:A:943:VAL:HG22	1:A:971:MET:HE1	1.84	0.59
1:C:990:PRO:HB2	1:C:994:ASP:HB2	1.84	0.58
1:D:883:LEU:HD21	1:D:928:GLU:HG2	1.86	0.58
1:C:961:PHE:HA	1:C:964:LEU:HD12	1.86	0.58
1:B:908:MET:CE	1:B:943:VAL:HG11	2.33	0.58
1:A:961:PHE:HA	1:A:964:LEU:HD12	1.86	0.57
1:C:796:GLY:HA2	2:C:1101:ZRT:C28	2.33	0.57
1:B:723:PHE:CB	1:B:745:LYS:CE	2.82	0.57
1:D:755:ALA:HB3	1:D:758:GLU:OE1	2.04	0.57
1:B:938:ILE:HG13	1:B:979:LEU:HD22	1.87	0.57
1:D:718:LEU:HD21	1:D:728:LYS:HB2	1.87	0.57
1:B:830:ASP:HB3	1:C:717:VAL:HG11	1.86	0.57
1:B:826:ASN:ND2	3:B:1205:HOH:O	2.39	0.56
1:B:884:GLU:OE2	1:B:958:ARG:NH1	2.23	0.56
1:C:729:GLY:HA3	1:C:744:ILE:HD12	1.88	0.56
1:C:962:ARG:NH2	1:C:966:ILE:CD1	2.49	0.56
1:B:726:VAL:HG22	1:B:745:LYS:HD3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:768:SER:OG	1:A:831:ARG:NH2	2.24	0.54
1:D:812:GLN:OE1	1:D:975:PRO:HG3	2.08	0.54
1:B:724:GLY:HA3	1:B:746:GLU:O	2.08	0.54
1:B:882:ALA:HA	1:B:898:TRP:CD2	2.43	0.53
1:B:715:ILE:HG22	1:B:716:LYS:HD2	1.91	0.53
1:B:747:LEU:O	1:B:785:THR:HB	2.08	0.52
1:B:752:SER:HB2	1:B:756:ASN:OD1	2.09	0.52
1:D:825:MET:CE	1:D:838:LEU:HD22	2.39	0.52
1:B:724:GLY:H	1:B:745:LYS:NZ	2.08	0.51
1:B:883:LEU:HD22	1:B:953:ILE:HD12	1.92	0.51
1:B:820:GLN:HE21	1:B:1010:VAL:HG21	1.76	0.51
1:B:877:PRO:O	1:B:881:MET:HG3	2.09	0.51
1:D:867:LYS:NZ	1:D:875:LYS:HG2	2.26	0.51
1:C:793:MET:CE	1:C:852:LYS:HD3	2.40	0.51
1:D:722:ALA:CB	1:D:875:LYS:HD2	2.23	0.50
1:D:715:ILE:HD11	1:D:730:LEU:HD12	1.94	0.50
1:D:1004:GLU:HB2	1:B:1004:GLU:HG3	1.93	0.50
1:D:908:MET:HG3	1:D:939:CYS:SG	2.52	0.50
1:C:832:ARG:NH1	3:C:1208:HOH:O	2.42	0.50
1:D:832:ARG:HG3	1:D:832:ARG:NH1	2.27	0.49
1:D:865:GLU:H	1:D:867:LYS:HD2	1.77	0.49
1:B:708:LYS:HG3	1:B:710:THR:HG22	1.94	0.49
1:A:924:SER:O	1:A:928:GLU:HG3	2.11	0.49
1:C:950:CYS:O	1:C:958:ARG:HD3	2.12	0.49
1:C:701:GLN:HA	1:C:764:TYR:CD1	2.47	0.49
1:D:1000:ALA:HB2	1:B:776:ARG:HH12	1.77	0.49
1:B:996:ASN:ND2	3:B:1202:HOH:O	2.27	0.49
1:B:831:ARG:CB	1:B:833:LEU:HD12	2.42	0.49
1:D:752:SER:O	1:D:753:PRO:C	2.51	0.48
1:D:809:ILE:HD12	1:D:817:TRP:HH2	1.78	0.48
1:B:720:SER:HB3	1:B:725:THR:HG23	1.95	0.48
1:B:925:SER:O	1:B:929:LYS:HG2	2.13	0.48
1:D:705:ARG:NH1	1:B:994:ASP:OD1	2.46	0.48
1:C:989:LEU:HB3	1:C:990:PRO:HD2	1.95	0.48
1:D:825:MET:HE2	1:D:838:LEU:HD13	1.96	0.48
1:B:782:LEU:HA	1:B:782:LEU:HD23	1.55	0.48
1:B:904:VAL:O	1:B:908:MET:HG2	2.14	0.48
1:D:929:LYS:N	1:D:929:LYS:HD3	2.28	0.48
1:A:998:TYR:CE1	1:A:1002:MET:SD	3.07	0.48
1:B:796:GLY:HA2	2:B:1101:ZRT:C28	2.43	0.48
1:B:745:LYS:HB3	1:B:788:LEU:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:877:PRO:HB2	1:B:880:TRP:HB2	1.94	0.47
1:D:804:GLU:OE1	1:D:805:HIS:CE1	2.67	0.47
1:A:812:GLN:HG2	1:A:975:PRO:HG3	1.96	0.47
1:C:986:ARG:HH11	1:C:986:ARG:CG	2.18	0.47
1:D:1001:LEU:HD21	1:B:742:VAL:HG12	1.95	0.47
1:B:835:HIS:C	1:B:836:ARG:HE	2.18	0.47
1:B:908:MET:HE3	1:B:943:VAL:HG11	1.96	0.47
1:D:948:ARG:HA	1:D:948:ARG:HD2	1.71	0.46
1:D:812:GLN:NE2	1:D:1011:VAL:O	2.49	0.46
1:B:766:MET:O	1:B:769:VAL:HG22	2.16	0.46
1:B:793:MET:CE	1:B:852:LYS:HD3	2.46	0.46
1:B:960:LYS:HA	1:B:960:LYS:HD2	1.65	0.46
1:B:724:GLY:N	1:B:745:LYS:HZ1	2.12	0.46
1:D:812:GLN:NE2	1:D:816:ASN:OD1	2.49	0.46
1:D:861:LEU:HD12	1:D:862:LEU:HD12	1.98	0.46
1:D:882:ALA:HA	1:D:898:TRP:CD2	2.51	0.45
1:C:701:GLN:CA	1:C:764:TYR:HE1	2.27	0.45
1:A:729:GLY:HA3	1:A:744:ILE:HD12	1.95	0.45
1:D:836:ARG:HG2	1:D:891:TYR:CG	2.51	0.45
1:A:846:LYS:NZ	1:C:1004:GLU:OE2	2.48	0.45
1:D:825:MET:HE3	1:D:838:LEU:HD22	1.98	0.45
1:B:762:GLU:O	1:B:766:MET:HG3	2.16	0.45
1:D:836:ARG:HG2	1:D:891:TYR:CD1	2.52	0.45
1:A:752:SER:HA	1:A:753:PRO:HD3	1.87	0.45
1:A:925:SER:OG	3:A:1101:HOH:O	2.21	0.45
1:D:976:GLN:NE2	3:D:1108:HOH:O	2.49	0.45
1:A:900:TYR:O	1:A:904:VAL:HG23	2.17	0.45
1:B:795:PHE:HB2	1:B:845:VAL:O	2.16	0.45
1:B:829:GLU:HG3	1:B:893:HIS:CG	2.52	0.45
1:B:990:PRO:HB2	1:B:994:ASP:HB2	1.98	0.44
1:B:750:ALA:O	1:B:752:SER:N	2.49	0.44
1:D:783:THR:OG1	1:D:784:SER:N	2.50	0.44
1:A:752:SER:O	1:A:754:LYS:N	2.46	0.44
1:C:793:MET:HE1	1:C:852:LYS:HD3	1.98	0.44
1:C:913:LYS:NZ	1:C:913:LYS:HB3	2.33	0.44
1:D:867:LYS:O	1:D:876:VAL:HG11	2.12	0.44
1:B:813:TYR:OH	1:B:990:PRO:HD3	2.18	0.44
1:C:772:PRO:O	1:C:850:HIS:NE2	2.51	0.44
1:C:783:THR:OG1	1:C:784:SER:N	2.49	0.44
1:C:803:ARG:HG3	1:C:911:GLY:HA3	2.00	0.44
1:D:755:ALA:O	1:D:759:ILE:HG13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:850:HIS:ND1	1:C:1003:ASP:OD2	2.34	0.44
1:C:882:ALA:HA	1:C:898:TRP:CD2	2.52	0.44
1:C:705:ARG:NH2	1:C:711:GLU:OE1	2.50	0.43
1:C:708:LYS:O	1:C:711:GLU:HG2	2.18	0.43
1:A:836:ARG:HG2	1:A:891:TYR:CD1	2.53	0.43
1:A:790:MET:HE3	1:A:790:MET:HB3	1.89	0.43
1:C:716:LYS:HE3	1:C:728:LYS:HD3	2.01	0.43
1:B:755:ALA:O	1:B:759:ILE:HD12	2.19	0.43
1:D:788:LEU:HD11	1:D:858:LEU:HD21	2.01	0.43
1:C:962:ARG:HD2	1:C:962:ARG:HA	1.68	0.42
1:D:751:THR:HG21	1:D:864:ALA:C	2.39	0.42
1:A:998:TYR:HE1	1:A:1002:MET:SD	2.41	0.42
1:B:723:PHE:CB	1:B:745:LYS:NZ	2.81	0.42
1:B:791:GLN:H	1:B:791:GLN:HG3	1.72	0.42
1:D:750:ALA:CB	1:D:862:LEU:HA	2.49	0.42
1:D:858:LEU:HD23	1:D:858:LEU:HA	1.87	0.42
1:D:1012:ASP:OD1	1:D:1012:ASP:N	2.53	0.42
1:B:725:THR:HB	1:B:727:TYR:CE1	2.55	0.42
1:B:714:LYS:HG2	1:B:727:TYR:CG	2.54	0.42
1:B:948:ARG:HA	1:B:948:ARG:HD2	1.85	0.42
1:A:882:ALA:HA	1:A:898:TRP:CD2	2.54	0.42
1:C:739:LYS:NZ	3:C:1213:HOH:O	2.52	0.42
1:D:905:TRP:HD1	1:D:947:MET:HE1	1.85	0.41
1:A:943:VAL:O	1:A:947:MET:HG3	2.19	0.41
1:D:823:LYS:HA	1:D:965:ILE:HD11	2.01	0.41
1:B:718:LEU:HD22	2:B:1101:ZRT:C25	2.49	0.41
1:B:999:ARG:HA	1:B:1003:ASP:HB3	2.01	0.41
1:C:829:GLU:HG3	1:C:893:HIS:HB3	2.02	0.41
1:A:750:ALA:C	1:A:752:SER:H	2.24	0.41
1:D:816:ASN:O	1:D:820:GLN:HG3	2.21	0.41
1:A:797:CYS:HA	1:A:844:LEU:HA	2.03	0.41
1:D:803:ARG:HG3	1:D:911:GLY:HA3	2.02	0.41
1:D:734:GLU:O	1:D:736:GLU:HG2	2.20	0.41
1:D:867:LYS:HZ3	1:D:867:LYS:HG2	1.66	0.41
1:D:962:ARG:NH2	1:A:718:LEU:O	2.54	0.41
1:D:811:SER:HB3	1:D:981:ILE:HD12	2.02	0.41
1:D:750:ALA:HB1	1:D:862:LEU:HA	2.03	0.41
1:A:745:LYS:HB3	1:A:788:LEU:HB2	2.03	0.41
1:B:746:GLU:HG3	1:B:787:GLN:HG2	2.02	0.41
1:D:962:ARG:NH2	1:A:719:GLY:HA2	2.36	0.40
1:D:825:MET:CE	1:D:838:LEU:HB2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:944:TYR:CZ	1:A:948:ARG:HD3	2.56	0.40
1:C:737:LYS:HD2	1:C:737:LYS:N	2.35	0.40
1:B:812:GLN:HG2	1:B:989:LEU:HD22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	300/328 (92%)	289 (96%)	9 (3%)	2 (1%)	22	43
1	B	288/328 (88%)	267 (93%)	17 (6%)	4 (1%)	11	22
1	C	282/328 (86%)	273 (97%)	8 (3%)	1 (0%)	34	57
1	D	295/328 (90%)	273 (92%)	19 (6%)	3 (1%)	15	32
All	All	1165/1312 (89%)	1102 (95%)	53 (4%)	10 (1%)	17	35

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	806	LYS
1	A	806	LYS
1	B	722	ALA
1	B	751	THR
1	B	753	PRO
1	D	923	ILE
1	A	783	THR
1	C	783	THR
1	B	783	THR
1	D	753	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	268/288 (93%)	260 (97%)	8 (3%)	41	67
1	B	257/288 (89%)	244 (95%)	13 (5%)	24	46
1	C	255/288 (88%)	240 (94%)	15 (6%)	19	39
1	D	267/288 (93%)	251 (94%)	16 (6%)	19	39
All	All	1047/1152 (91%)	995 (95%)	52 (5%)	25	47

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	713	LYS
1	D	734	GLU
1	D	748	ARG
1	D	749	GLU
1	D	757	LYS
1	D	761	ASP
1	D	804	GLU
1	D	825	MET
1	D	867	LYS
1	D	868	GLU
1	D	876	VAL
1	D	922[A]	GLU
1	D	922[B]	GLU
1	D	925	SER
1	D	970	LYS
1	D	1012	ASP
1	A	705	ARG
1	A	734	GLU
1	A	889	ARG
1	A	962	ARG
1	A	995	SER
1	A	998	TYR
1	A	1005	GLU
1	A	1012	ASP

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Mol	Chain	Res	Type
1	B	705	ARG
1	B	749	GLU
1	B	754	LYS
1	B	784	SER
1	B	790	MET
1	B	800	ASP
1	B	806	LYS
1	B	833	LEU
1	B	956	ASP
1	B	977	ARG
1	B	986	ARG
1	B	1002	MET
1	B	1010	VAL
1	C	701	GLN
1	C	745	LYS
1	C	757	LYS
1	C	761	ASP
1	C	806	LYS
1	C	808	ASN
1	C	855	ASP
1	C	921	SER
1	C	924	SER
1	C	945	MET
1	C	960	LYS
1	C	962	ARG
1	C	987	MET
1	C	995	SER
1	C	998	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	805	HIS
1	D	976	GLN
1	A	988	HIS
1	B	812	GLN
1	B	826	ASN
1	C	756	ASN
1	C	808	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ZRT	B	1101	1	43,45,45	1.58	7 (16%)	53,62,62	2.02	11 (20%)
2	ZRT	C	1101	1	43,45,45	1.51	7 (16%)	53,62,62	1.95	11 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ZRT	B	1101	1	-	6/25/36/36	0/5/5/5
2	ZRT	C	1101	1	-	7/25/36/36	0/5/5/5

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1101	ZRT	C30-N29	4.59	1.45	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1101	ZRT	C30-N29	4.49	1.45	1.35
2	B	1101	ZRT	C33-C32	-4.31	1.32	1.51
2	B	1101	ZRT	C18-N22	4.27	1.45	1.36
2	C	1101	ZRT	C18-N22	3.66	1.44	1.36
2	B	1101	ZRT	C10-C09	3.04	1.52	1.49
2	C	1101	ZRT	C09-N08	-2.77	1.33	1.35
2	C	1101	ZRT	C10-C09	2.64	1.52	1.49
2	C	1101	ZRT	C18-N19	-2.45	1.31	1.34
2	B	1101	ZRT	C27-N29	2.38	1.46	1.41
2	C	1101	ZRT	O31-C30	-2.37	1.18	1.23
2	C	1101	ZRT	C26-N34	2.18	1.46	1.41
2	B	1101	ZRT	O31-C30	-2.17	1.18	1.23
2	B	1101	ZRT	C09-N08	-2.17	1.33	1.35

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1101	ZRT	C20-N19-C18	7.41	122.02	115.45
2	C	1101	ZRT	C20-N19-C18	7.21	121.84	115.45
2	B	1101	ZRT	N19-C18-N17	-5.14	121.68	126.55
2	C	1101	ZRT	C33-C32-C30	5.03	129.28	113.30
2	B	1101	ZRT	C21-C20-N19	-4.72	118.10	123.96
2	C	1101	ZRT	N19-C18-N17	-4.62	122.17	126.55
2	C	1101	ZRT	C21-C20-N19	-4.51	118.35	123.96
2	B	1101	ZRT	O40-C24-C23	4.42	120.23	114.80
2	C	1101	ZRT	O40-C24-C23	4.10	119.83	114.80
2	B	1101	ZRT	C25-C26-N34	-3.60	117.20	122.52
2	B	1101	ZRT	C41-O40-C24	-3.54	112.18	117.53
2	B	1101	ZRT	O40-C24-C25	-2.65	119.56	124.12
2	C	1101	ZRT	C41-O40-C24	-2.59	113.63	117.53
2	B	1101	ZRT	C39-N34-C35	-2.42	106.18	111.52
2	C	1101	ZRT	O40-C24-C25	-2.39	120.00	124.12
2	B	1101	ZRT	C38-O37-C36	2.29	117.53	109.89
2	C	1101	ZRT	C39-N34-C35	-2.26	106.52	111.52
2	C	1101	ZRT	C25-C26-N34	-2.24	119.20	122.52
2	C	1101	ZRT	C39-N34-C26	2.23	121.56	116.27
2	B	1101	ZRT	C33-C32-C30	2.18	120.23	113.30
2	B	1101	ZRT	C23-N22-C18	-2.05	123.42	129.60
2	C	1101	ZRT	C10-C09-N08	2.00	124.21	120.78

There are no chirality outliers.

All (13) torsion outliers are listed below:

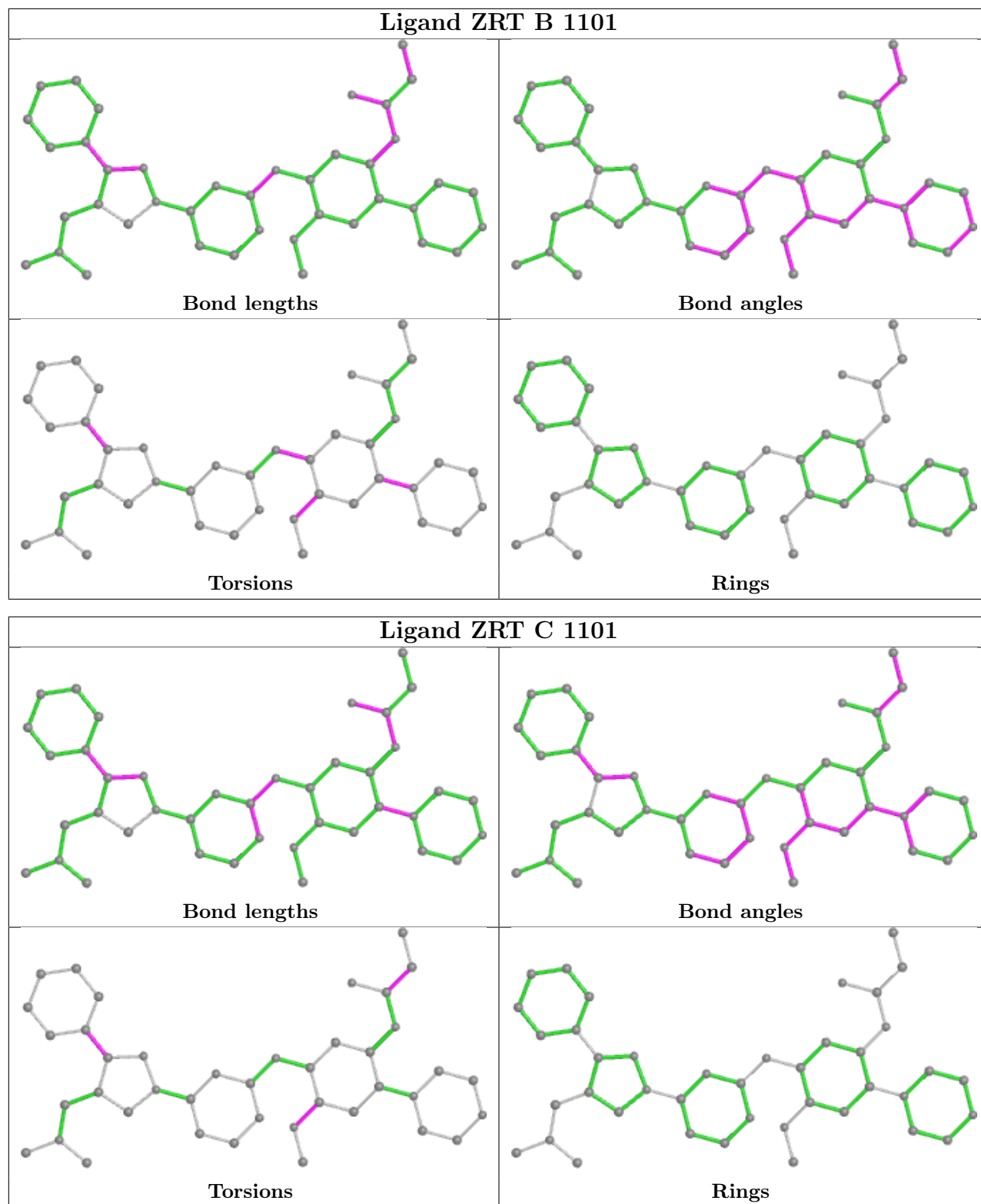
Mol	Chain	Res	Type	Atoms
2	C	1101	ZRT	N08-C09-C10-C11
2	C	1101	ZRT	N08-C09-C10-C15
2	B	1101	ZRT	C23-C24-O40-C41
2	B	1101	ZRT	C25-C24-O40-C41
2	C	1101	ZRT	C23-C24-O40-C41
2	C	1101	ZRT	C25-C24-O40-C41
2	B	1101	ZRT	C25-C26-N34-C39
2	B	1101	ZRT	C25-C26-N34-C35
2	C	1101	ZRT	N29-C30-C32-C33
2	C	1101	ZRT	O31-C30-C32-C33
2	B	1101	ZRT	C28-C23-N22-C18
2	B	1101	ZRT	C05-C09-C10-C11
2	C	1101	ZRT	C05-C09-C10-C15

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1101	ZRT	3	0
2	C	1101	ZRT	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	306/328 (93%)	-0.04	8 (2%) 56 50	26, 40, 65, 82	0
1	B	292/328 (89%)	0.03	13 (4%) 33 26	28, 44, 74, 100	0
1	C	287/328 (87%)	-0.06	8 (2%) 53 46	24, 43, 69, 90	0
1	D	300/328 (91%)	-0.05	4 (1%) 77 73	24, 41, 72, 88	0
All	All	1185/1312 (90%)	-0.03	33 (2%) 53 46	24, 42, 70, 100	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1008	ASP	4.2
1	B	988	HIS	4.1
1	B	751	THR	3.9
1	B	1009	ASP	3.8
1	D	751	THR	3.5
1	B	858	LEU	3.5
1	B	989	LEU	3.2
1	B	1010	VAL	3.2
1	C	860	LYS	3.1
1	A	917	GLY	3.1
1	C	722	ALA	3.0
1	C	858	LEU	2.9
1	A	783	THR	2.8
1	C	988	HIS	2.7
1	C	760	LEU	2.7
1	B	786	VAL	2.7
1	A	868	GLU	2.7
1	B	782	LEU	2.6
1	A	782	LEU	2.6
1	C	859	ALA	2.5
1	B	723	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	748	ARG	2.4
1	C	756	ASN	2.3
1	A	807	ASP	2.3
1	D	988	HIS	2.3
1	A	708	LYS	2.3
1	D	866	GLU	2.3
1	D	807	ASP	2.3
1	B	749	GLU	2.2
1	C	928	GLU	2.1
1	A	867	LYS	2.1
1	B	1007	MET	2.0
1	A	988	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

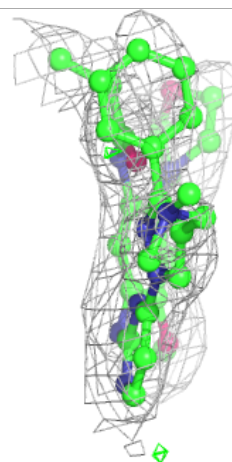
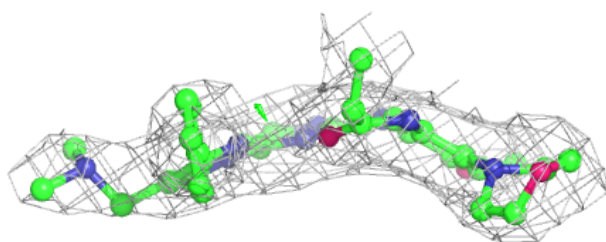
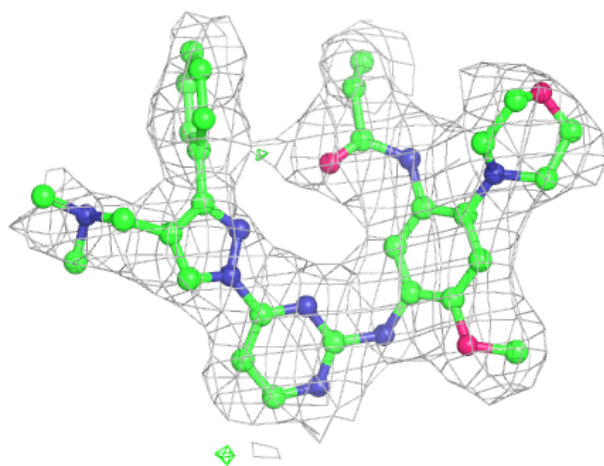
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

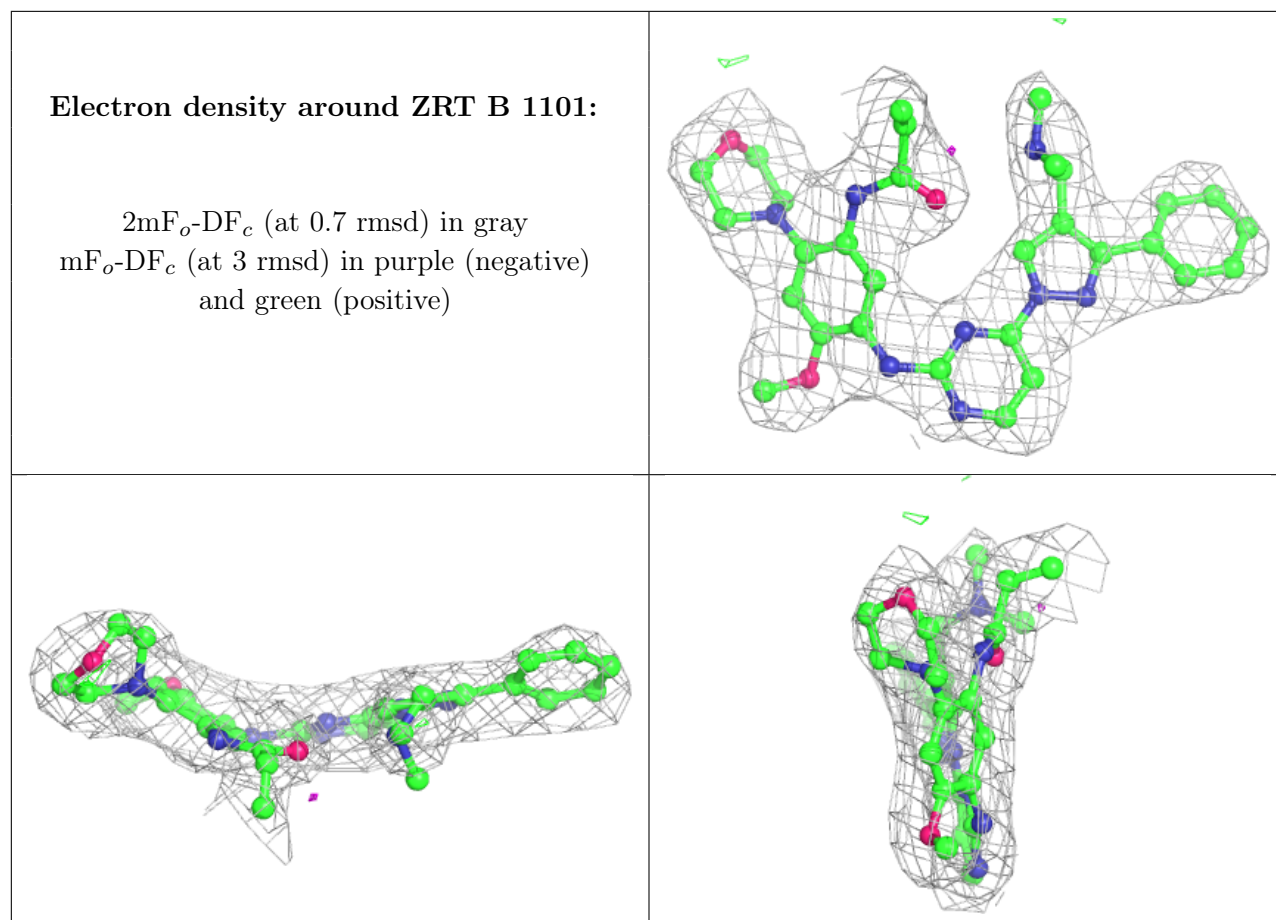
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZRT	C	1101	41/41	0.91	0.16	33,46,64,70	0
2	ZRT	B	1101	41/41	0.94	0.15	24,37,47,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ZRT C 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.